

Patent claims:

1. A degenerate primer constituent from the group consisting of
 - 5 A-01f : gcsmrsgcstgg (Seq. ID NO. 1)
 - B-01f : ggsctscscsc (Seq. ID NO. 2)
 - B-01r : ggs ggsagscc (Seq. ID NO. 3)
 - C-01r : ggn cgcwbsgg (Seq. ID NO. 4)
 - A-01f : gcnmrrgcntgg (Seq. ID NO. 5)
 - 10 B-01f : ggnytnccncc (Seq. ID NO. 6)
 - B-01r : ggnggnarncc (Seq. ID NO. 7)
 - C-01r : gwn gwr tccca (Seq. ID NO. 8)
 - A-01f : gcntggrynga (Seq. ID NO. 9)
 - B-01f : ggnytsccncc (Seq. ID NO. 10)
 - 15 B-01r : ggnggsarncc (Seq. ID NO. 11)
 - C-01r : swns wr tccca (Seq. ID NO. 12).
2. A process for preparing protein sequences which are required for constructing the activity of a nitrile
20 hydratase, such that
 - a) a metagenome DNA library of a habitat is prepared,
 - b) this library is contacted with in each case at least one forward(f) primer and one reverse(r) primer exhibiting a degenerate nucleic acid sequence as
25 claimed in claim 1,
 - c) a PCR is carried out using these primers,
 - d) the full-length sequences of the nucleic acids encoding protein sequences which are required for constructing the activity of a nitrile hydratase are
30 generated from the part sequences which are obtained, and
 - e) these full-length sequences are cloned into a host organism and expressed.
- 35 3. The process as claimed in claim 2, characterized in that

in each case primer pairs composed of primers exhibiting the nucleic acid sequences A-01f and B-01r or C-01r and also B-01f and C-01r are used in the PCR.

- 5 4. The process as claimed in claim 2 and/or 3, characterized in that nucleic acid sequences selected from the group consisting of:

	GCCAAGGTCGTC	(Seq. ID NO. 13)
10	GGCCGGTCCTG	(Seq. ID NO. 14)
	TCCTTGTACCAGGTC	(Seq. ID NO. 15)
	GCCCGCC	(Seq. ID NO. 16)
	GGCGCTAATGTTGTT	(Seq. ID NO. 17)
	TGGCCGGTTCTG	(Seq. ID NO. 18)
15	CAAATTCTTTATACCAAGTC	(Seq. ID NO. 19)
	CCATATATCGCATTTTCAGCT	(Seq. ID NO. 20)
	GGTCGTGGCCAAG	(Seq. ID NO. 21)
	GGCCGGTCCTG	(Seq. ID NO. 22)
	TCCTTGTACCAGGTC	(Seq. ID NO. 23)
20	GCGCATTTTCGGCG	(Seq. ID NO. 24)

are placed upstream of the degenerate nucleic acid sequences.

- 25 5. The process as claimed in one or more of the preceding claims 2 to 4, characterized in that use is made of primers which are selected from the group consisting of

	GCCAAGGTCGTC <u>gcsmrsgcstgg</u>	(Seq. ID NO. 25)
30	GGCCGGTCCTG <u>ggsctscscscc</u>	(Seq. ID NO. 26)
	TCCTTGTACCAGGTC <u>ggsagsagscc</u>	(Seq. ID NO. 27)
	GCCCGCC <u>ggncgcwbsgg</u>	(Seq. ID NO. 28)
	GGCGCTAAAGTTGTT <u>gcnmrrgcntgg</u>	(Seq. ID NO. 29)
	TGGCCGGTTCTG <u>ggnytnccncc</u>	(Seq. ID NO. 30)
35	CAAATTCTTTATACCAAGTC <u>ggnggnarncc</u>	(Seq. ID NO. 31)
	CCATATATCGCATTTTCAGCT <u>gwngrwtccca</u>	(Seq. ID NO. 32)
	GGTCGTGGCCAAG <u>gcntggrynga</u>	(Seq. ID NO. 33)

GGCCGGTCCTGggnytsccncc (Seq. ID NO. 34)
TCCTTGTACCAGGTCggnggsarncc (Seq. ID NO. 35)
GCGCATTTTCGGCGswns wrtccca (Seq. ID NO. 36).

- 5 6. A protein sequence which is required for constructing
the activity of a nitrile hydratase and which has less
than 100% homology, at the amino acid level, with such
known protein sequences, with the nucleic acid
sequences encoding it being generated from part
10 sequences which give a positive hybridization signal,
under stringent conditions, with the primers
exhibiting the nucleic acid sequences of claim 1.
- 15 7. A nucleic acid sequence which encodes a protein
sequence as claimed in claim 6.
8. An expression system which exhibits one or more
nucleic acid sequences as claimed in claim 7.
- 20 9. A nitrile hydratase which exhibits protein sequences
for α subunits and β subunits as claimed in claim 6.
- 25 10. The use of the nucleic acid sequences as claimed in
claim 7 for producing improved protein sequences which
are required for constructing the activity of a
nitrile hydratase.
11. The use of the nitrile hydratases as claimed in
claim 9 for preparing organic acid amides and acids.